

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Yue, Henry
Corley, Neil C.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0451 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 545 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TLYMNOT05
 - (B) CLONE: 2809795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Thr Glu His Val Asn Gly Asn Gly Thr Glu Glu Pro Met Asp
 1 5 10 15
 Thr Thr Ser Ala Val Ile His Ser Glu Asn Phe Gln Thr Leu Leu Asp
 20 25 30
 Ala Gly Leu Pro Gln Lys Val Ala Glu Lys Leu Asp Glu Ile Tyr Val
 35 40 45
 Ala Gly Leu Val Ala His Ser Asp Leu Asp Glu Arg Ala Ile Glu Ala
 50 55 60
 Leu Lys Glu Phe Asn Glu Asp Gly Ala Leu Ala Val Leu Gln Gln Phe
 65 70 75 80
 Lys Asp Ser Asp Leu Ser His Val Gln Asn Lys Ser Ala Phe Leu Cys
 85 90 95
 Gly Val Met Lys Thr Tyr Arg Gln Arg Glu Lys Gln Gly Thr Lys Val
 100 105 110
 Ala Asp Ser Ser Lys Gly Pro Asp Glu Ala Lys Ile Lys Ala Leu Leu
 115 120 125
 Glu Arg Thr Gly Tyr Thr Leu Asp Val Thr Thr Gly Gln Arg Lys Tyr
 130 135 140
 Gly Gly Pro Pro Pro Asp Ser Val Tyr Ser Gly Gln Gln Pro Ser Val
 145 150 155 160
 Gly Thr Glu Ile Phe Val Gly Lys Ile Pro Arg Asp Leu Phe Glu Asp
 165 170 175
 Glu Leu Val Pro Leu Phe Glu Lys Ala Gly Pro Ile Trp Asp Leu Arg
 180 185 190
 Leu Met Met Asp Pro Leu Thr Gly Leu Asn Arg Gly Tyr Ala Phe Val
 195 200 205
 Thr Phe Cys Thr Lys Glu Ala Ala Gln Glu Ala Val Lys Leu Tyr Asn
 210 215 220
 Asn His Glu Ile Arg Ser Gly Lys His Ile Gly Val Cys Ile Ser Val
 225 230 235 240
 Ala Asn Asn Arg Leu Phe Val Gly Ser Ile Pro Lys Ser Lys Thr Lys
 245 250 255
 Glu Gln Ile Leu Glu Glu Phe Ser Lys Val Thr Glu Gly Leu Thr Asp
 260 265 270
 Val Ile Leu Tyr His Gln Pro Asp Lys Lys Lys Asn Arg Gly Phe
 275 280 285
 Cys Phe Leu Glu Tyr Glu Asp His Lys Thr Ala Ala Gln Ala Arg Arg
 290 295 300
 Arg Leu Met Ser Gly Lys Val Lys Val Trp Gly Asn Val Gly Thr Val
 305 310 315 320
 Glu Trp Ala Asp Pro Ile Glu Asp Pro Asp Pro Glu Val Met Ala Lys
 325 330 335
 Val Lys Val Leu Phe Val Arg Asn Leu Ala Asn Thr Val Thr Glu Glu
 340 345 350
 Ile Leu Glu Lys Ala Phe Ser Gln Phe Gly Lys Leu Glu Arg Val Lys
 355 360 365
 Lys Leu Lys Asp Tyr Ala Phe Ile His Phe Asp Glu Arg Asp Gly Ala
 370 375 380
 Val Lys Ala Met Glu Glu Met Asn Gly Lys Asp Leu Glu Gly Glu Asn
 385 390 395 400
 Ile Glu Ile Val Phe Ala Lys Pro Pro Asp Gln Lys Arg Lys Glu Arg
 405 410 415
 Lys Ala Gln Arg Gln Ala Ala Lys Asn Gln Met Tyr Asp Asp Tyr Tyr
 420 425 430
 Tyr Tyr Gly Pro Pro His Met Pro Pro Pro Thr Arg Gly Arg Gly Arg
 435 440 445
 Gly Gly Arg Gly Gly Tyr Gly Tyr Pro Pro Asp Tyr Tyr Gly Tyr Glu
 450 455 460

Asp Tyr Tyr Asp Tyr Tyr Gly Tyr Asp Tyr His Asn Tyr Arg Gly Gly
 465 470 475 480
 Tyr Glu Asp Pro Tyr Tyr Gly Tyr Glu Asp Phe Gln Val Gly Ala Arg
 485 490 495
 Gly Arg Gly Gly Arg Gly Ala Arg Gly Ala Ala Pro Ser Arg Gly Arg
 500 505 510
 Gly Ala Ala Pro Pro Arg Gly Arg Ala Gly Tyr Ser Gln Arg Gly Gly
 515 520 525
 Pro Gly Ser Ala Arg Gly Val Arg Ala Gly Lys Arg Gly Arg Gly Arg
 530 535 540
 Ser
 545

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TLYMNOT05
- (B) CLONE: 2809795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGCGCGCGC	GCGCACCGGG	AGCGCGCTCG	GAGGCGAGTG	GAACCTGGATC	GGGTTTGCTG	60
CCAGCGGCGT	GAGCTTCGGC	CGGCATTTTA	CAACAGCTCC	ACTCGCGCCG	GACACAGGGA	120
GCAGCGAGCA	CGCGTTTCCC	GCAACCCGAT	ACCATCGGAC	AGGATTTCTC	CGCCTCAGCC	180
CAACGGGGAG	ATCTCTGGAA	ACATGGCTAC	AGAACATGTT	AATGGAAATG	GTAAGTGAAGA	240
GCCCATGGAT	ACTACTTCTG	CAGTTATCCA	TTCAGAAAAT	TTTCAGACAT	TGCTTGATGC	300
TGGTTTACCA	CAGAAAGTTG	CTGAAAAACT	AGATGAAATT	TACGTTGCAG	GGCTAGTTGC	360
ACATAGTGAT	TTAGATGAAA	GAGCTATTGA	AGCTTTAAAA	GAATTCATG	AAGACGGTGC	420
ATTGGCAGTT	CTTCAACAGT	TTAAAGACAG	TGATCTCTCT	CATGTTTCAG	ACAAAAGTGC	480
CTTTTATGT	GGAGTCATGA	AGACTTACAG	GCAGAGAGAA	AAACAAGGGA	CCAAAAGTAGC	540
AGATTCTAGT	AAAGGACCAG	ATGAGGCAAA	AATTAAGGCA	CTCTTGGAAG	GAACAGGCTA	600
CACACTTGAT	GTGACCACTG	GACAGAGGAA	GTATGGAGGA	CCACCTCCAG	ATTCCGTTTA	660
TTCAGGTCAG	CAGCCTTCTG	TTGGCACTGA	GATATTTGTG	GGAAAGATCC	CAAGAGATCT	720
ATTTGAGGAT	GAACCTGTTC	CATTATTTGA	GAAAGCTGGA	CCTATATGGG	ATCTTCGTCT	780
AATGATGGAT	CCACTCACTG	GTCTCAATAG	AGGTTATGCG	TTTGTCACTT	TTGTACAAA	840
AGAAGCAGCT	CAGGAGGCTG	TTAAACTGTA	TAATAATCAT	GAAATTCGTT	CTGGAAAACA	900
TATTGGTGTC	TGCATCTCAG	TTGCCAACAA	TAGGCTTTTT	GTGGGCTCTA	TTCTTAAGAG	960
TAAAACCAAG	GAACAGATTG	TTGAAGAATT	TAGCAAAGTA	ACAGAGGGTC	TTACAGACGT	1020
CATTTTATAC	CACCAACCGG	ATGACAAGAA	AAAAACAGA	GGCTTTTGCT	TTCTTGAATA	1080
TGAAGATCAC	AAAACAGCTG	CCCAGGCAAG	GCGTAGGTTA	ATGAGTGGA	AAGTCAAGGT	1140
CTGGGGGAAT	GTTGGAACGT	TTGAATGGGC	TGATCCTATA	GAAGATCCTG	ATCCTGAGGT	1200
TATGGCAAAAG	GTAAAAGTGC	TGTTTGACG	CAACCTTGCC	AATACGTAA	CAGAAGAGAT	1260
TTTAGAAAAG	GCATTTAGTC	AGTTTGGGAA	ACTGGAACGA	GTGAAGAAGT	TAAAAGATTA	1320
TGCGTTCATT	CATTTTGATG	AGCGAGATGG	TGCTGTCAAG	GCTATGGAAG	AAATGAATGG	1380
CAAGAGACTTG	GAGGGAGAAA	ATATTGAAAT	TGTTTTTGCC	AAGCCACCAG	ATCAGAAAAG	1440
GAAAGAAAGA	AAAGCTCAGA	GGCAAGCAGC	AAAAAATCAA	ATGTATGACG	ATTACTACTA	1500
TTATGGTCCA	CCTCATATGC	CCCCCCAAC	AAGAGGTCGA	GGGCGTGGAG	GTAAGAGTGG	1560
TTATGGATAT	CCTCCAGATT	ATTATGGATA	TGAAGATTAT	TATGATTATT	ATGGTTATGA	1620
TTACCATAAC	TATCGTGGTG	GATATGAAGA	TCCATACTAT	GGTTATGAAG	ATTTTCAAGT	1680
TGGAGCTAGA	GGAAGGGGTG	GTAAGGAGC	AAGGGGTGCT	GCTCCATCCA	GAGGTCGTGG	1740
GGCTGCTCCT	CCCCGCGGTA	GAGCCGGTTA	TTCACAGAGA	GGAGGTCCTG	GATCAGCAAG	1800
AGGCGTTCGA	GCAGGGAAAA	GGGGTCGAGG	CCGGTCCTGA	CCTGTTACAA	TGAAGACTGA	1860
CTTGCTATGT	GGGATTACAC	CAGAAGCTTG	CAGTGAGATA	ATGGTAAGGA	AATCAAGCAA	1920

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CCTTAAATAT	GTCGGCTGTA	TAGGAGCATA	TTCTATTGCA	GAAGACCTTC	CTATGAAGAT	1980
CATGGAATCA	AATACGGGAC	ATTGAACTAA	TACTTGGACT	TTGATATGAA	TTTCTTTAAC	2040
AATTTTCTCT	GCAGTGAAG	TTATTAAACT	AAAGCTACT			2079

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 128842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Val	Lys	Leu	Ala	Lys	Ala	Gly	Lys	Thr	His	Gly	Glu	Ala	Lys	Lys
1				5					10					15	
Met	Ala	Pro	Pro	Pro	Lys	Glu	Val	Glu	Glu	Asp	Ser	Glu	Asp	Glu	Glu
			20					25					30		
Met	Ser	Glu	Glu	Glu	Asp	Asp	Ser	Ser	Gly	Glu	Glu	Val	Val	Ile	Pro
		35					40					45			
Gln	Lys	Lys	Gly	Lys	Lys	Ala	Thr	Ala	Thr	Pro	Ala	Lys	Lys	Val	Val
		50				55					60				
Val	Ser	Gln	Thr	Lys	Lys	Val	Ala	Val	Pro	Thr	Pro	Ala	Lys	Lys	Ala
		65				70				75				80	
Ala	Val	Thr	Pro	Gly	Lys	Lys	Ala	Ala	Ala	Thr	Pro	Ala	Lys	Lys	Ala
				85					90					95	
Val	Thr	Pro	Ala	Lys	Ala	Val	Ala	Thr	Pro	Gly	Lys	Lys	Gly	Ala	Thr
			100					105					110		
Gln	Ala	Lys	Ala	Leu	Val	Ala	Thr	Pro	Gly	Lys	Lys	Gly	Ala	Val	Thr
		115					120					125			
Pro	Ala	Lys	Gly	Ala	Lys	Asn	Gly	Lys	Asn	Ala	Lys	Lys	Glu	Asp	Ser
		130				135					140				
Asp	Glu	Asp	Glu	Asp	Asp	Asp	Asp	Asp	Glu	Asp	Asp	Ser	Asp	Glu	Asp
		145				150				155				160	
Glu	Glu	Asp	Glu	Glu	Glu	Asp	Glu	Phe	Glu	Pro	Pro	Val	Val	Lys	Gly
			165					170						175	
Lys	Gln	Gly	Lys	Val	Ala	Ala	Ala	Ala	Pro	Ala	Ser	Glu	Asp	Glu	Asp
			180					185					190		
Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Asp
		195						200				205			
Asp	Ser	Glu	Glu	Glu	Glu	Ala	Met	Glu	Ile	Thr	Pro	Ala	Lys	Gly	Lys
		210				215					220				
Lys	Ala	Pro	Ala	Lys	Val	Val	Pro	Val	Lys	Ala	Lys	Asn	Val	Ala	Glu
				225		230				235				240	
Glu	Asp	Asp	Asp	Asp	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Glu	Asp	Glu
			245						250					255	
Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu
			260					265					270		
Pro	Val	Lys	Pro	Ala	Pro	Gly	Lys	Arg	Lys	Lys	Glu	Met	Thr	Lys	Gln
			275				280					285			
Lys	Glu	Val	Pro	Glu	Ala	Lys	Lys	Gln	Lys	Val	Glu	Gly	Ser	Glu	Ser
		290				295					300				
Thr	Thr	Pro	Phe	Asn	Leu	Phe	Ile	Gly	Asn	Leu	Asn	Pro	Asn	Lys	Ser
				305		310				315				320	
Val	Ala	Glu	Leu	Lys	Val	Ala	Ile	Ser	Glu	Pro	Phe	Ala	Lys	Asn	Asp
				325					330					335	

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Leu	Ala	Val	Val	Asp	Val	Arg	Thr	Gly	Thr	Asn	Arg	Lys	Phe	Gly	Tyr
			340					345					350		
Val	Asp	Phe	Glu	Ser	Ala	Glu	Asp	Leu	Glu	Lys	Ala	Leu	Glu	Leu	Thr
		355					360					365			
Gly	Leu	Lys	Val	Phe	Gly	Asn	Glu	Ile	Lys	Leu	Glu	Lys	Pro	Lys	Gly
	370					375					380				
Arg	Asp	Ser	Lys	Lys	Val	Arg	Ala	Ala	Arg	Thr	Leu	Leu	Ala	Lys	Asn
385					390					395					400
Leu	Ser	Phe	Asn	Ile	Thr	Glu	Asp	Glu	Leu	Lys	Glu	Val	Phe	Glu	Asp
			405					410						415	
Ala	Leu	Glu	Ile	Arg	Leu	Val	Ser	Gln	Asp	Gly	Lys	Ser	Lys	Gly	Ile
			420					425					430		
Ala	Tyr	Ile	Glu	Phe	Lys	Ser	Glu	Ala	Asp	Ala	Glu	Lys	Asn	Leu	Glu
		435					440					445			
Glu	Lys	Gln	Gly	Ala	Glu	Ile	Asp	Gly	Arg	Ser	Val	Ser	Leu	Tyr	Tyr
	450					455					460				
Thr	Gly	Glu	Lys	Gly	Gln	Arg	Gln	Glu	Arg	Thr	Gly	Lys	Asn	Ser	Thr
465					470					475					480
Trp	Ser	Gly	Glu	Ser	Lys	Thr	Leu	Val	Leu	Ser	Asn	Leu	Ser	Tyr	Ser
			485					490						495	
Ala	Thr	Glu	Glu	Thr	Leu	Gln	Glu	Val	Phe	Glu	Lys	Ala	Thr	Phe	Ile
			500					505					510		
Lys	Val	Pro	Gln	Asn	Gln	Gln	Gly	Lys	Ser	Lys	Gly	Tyr	Ala	Phe	Ile
		515					520					525			
Glu	Phe	Ala	Ser	Phe	Glu	Asp	Ala	Lys	Glu	Ala	Leu	Asn	Ser	Cys	Asn
	530					535					540				
Lys	Met	Glu	Ile	Glu	Gly	Arg	Thr	Ile	Arg	Leu	Glu	Leu	Gln	Gly	Pro
545					550					555					560
Arg	Gly	Ser	Pro	Asn	Ala	Arg	Ser	Gln	Pro	Ser	Lys	Thr	Leu	Phe	Val
			565					570						575	
Lys	Gly	Leu	Ser	Glu	Asp	Thr	Thr	Glu	Glu	Thr	Leu	Lys	Glu	Ser	Phe
			580					585					590		
Glu	Gly	Ser	Val	Arg	Ala	Arg	Ile	Val	Thr	Asp	Arg	Glu	Thr	Gly	Ser
		595					600					605			
Ser	Lys	Gly	Phe	Gly	Phe	Val	Asp	Phe	Asn	Ser	Glu	Glu	Asp	Ala	Lys
	610					615					620				
Ala	Ala	Lys	Glu	Ala	Met	Glu	Asp	Gly	Glu	Ile	Asp	Gly	Asn	Lys	Val
625					630					635					640
Thr	Leu	Asp	Trp	Ala	Lys	Pro	Lys	Gly	Glu	Gly	Gly	Phe	Gly	Gly	Arg
			645					650						655	
Gly	Gly	Gly	Arg	Gly	Gly	Phe	Gly	Gly	Arg	Gly	Gly	Gly	Arg	Gly	Gly
			660					665					670		
Gly	Arg	Gly	Gly	Phe	Gly	Gly	Arg	Gly	Arg	Gly	Gly	Phe	Gly	Gly	Arg
		675					680					685			
Gly	Gly	Phe	Arg	Gly	Gly	Arg	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Asp	Phe
	690					695					700				
Lys	Pro	Gln	Gly	Lys	Lys	Thr	Lys	Phe	Glu						
705					710										